REMARKS

Claim 8 remain in this application. Claims 1-7, 9 and 10 have been amended by eliminating multiple dependent claims and deleting preferably clauses. Attached hereto is a marked-up version of the changes made to the claims by the current amendment. The attached page is captioned "Version With Markings to Show Changes Made".

The support for these amendments is found in the claims as originally filed. These amendments are being entered to bring the claims into conformance with, *inter alia*, 37 CFR §1.75; no new matter is added.

Respectfully submitted,

By _____

T. David Reed
Agent for Applicants
Registration No. 32,931

09 July 2001
5299 Spring Grove Avenue
Cincinnati, Ohio 45217-1087
Phone: (513) 627-7025
FAX: (513) 627-6333

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the claims:

1. A method of determining the amino acid sequence of a polypeptide characterized in that it comprises:

(d) derivatizing the N-terminus of the polypeptide or the N-termini of one or more peptides of the polypeptide with one or more acidic moieties having pKas of less than 2[, preferably less than 0, more preferably less than –2] when coupled with the polypeptide or peptides, to provide one or more derivatized analytes;

(e) analyzing one or more derivatized analytes using a mass spectrometric technique to provide a fragmentation pattern[, preferably the fragmentation pattern is substantially free of a-ions and b-ions]; and

(f) interpreting the fragmentation pattern.

2. A method according to Claim 1 characterized in that the mass spectrometric technique is MALDI PSD mass spectrometry[, preferably positive ion mode PSD MALDI]; or electrospray ionization tandem mass spectrometry[, preferably tandem electrospray ionization mass spectrometry].

3. A method according to Claim [1 or] 2 characterized in that interpretation of the fragmentation pattern comprises using a commercially available software program or database.

4. A method according to Claim 3 [any of Claims 1-3] characterized in that the polypeptide is a synthetic polypeptide.

5. A method according to Claim 4 [any of Claims 1-4] characterized in that the peptides of the polypeptide are produced by digestion[, preferably the digestion is chemical digestion, more preferably the chemical digestion is cyanogen bromide digestion].

6. A method according to Claim 5 characterized in that the digestion is enzymatic digestion[, preferably the enzymatic digestion is selected from endoproteinase Lys C digestion, endoproteinase Arg C digestion, tryptic digestion, and chymotryptic digestion].

7. A method according to Claim 6 [any of Claims 1-6] characterized in that the acidic moiety is one or more sulfonic acids or a disulfonic acid derivative[, preferably the acidic moiety is a 2-sulfoacetyl moiety, a 3-sulfopropionoyl moiety, or a 2-sulfobenzoyl moiety].

8. A kit for use in determining the amino acid sequence of a polypeptide characterized in that it comprises:

(a) one or more acidic moiety reagents providing one or more acidic moieties having pKas of less than 2 when coupled with the polypeptide or one or more peptides of the polypeptide; and

(b) means for derivatizing the N-terminus of the polypeptide or the N-termini of one or more peptides of the polypeptide with one or more acidic moiety reagents.

9. A kit according to Claim 8 characterized in that the means for derivatizing comprises one or more containment devices[, preferably the acidic moiety reagent resides within the containment devices; preferably the means for derivatizing further comprises a buffer system].

10. A kit according to Claim [8 or] 9 characterized in that it further comprises one or more digestion aids.